

Name : Beg-zeBo-l e: 1 : 1396 Mode : Normal n Table : UniverBal

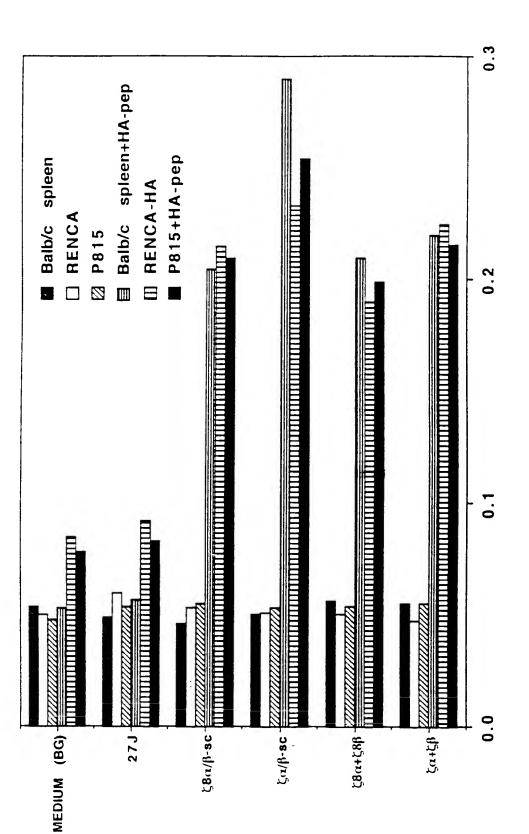
FIGURE 3A _ <

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XL		9			18						36			45			54
CTC	GAG	ATG	CAG	AGG	AAC	CTG	GGA	GCT	GTG	CTG	GGG	ATT	CTG	TGG	GTG	CAG	ATT
Ľ.	E	м	Q	R	N	L	G	A	v	L	G	I	L	W	v	Q	I
		63			72			81			90			99			108
TGC	TGG	CTG	AAA	GAA	CAG	CAA	GTG	CAG	CAG	AGT	CCC	GCA	TCC	TTG	GTT	CTG	CAG
С	w	L	к	E	Q	Q	v	Q	Q	s	P	A	s	L	V	L	Q
CNC	666	117		GCA	126	ame.	CAC	135	200	com co	144	አመሮ	mem m	153	AAC	CAG	162 GTG
Ε	G	E	11	A	E	L	Q	С	S	F	s	I	F	T	N	Q	V
		171			180	~~~		189				200		207	m a C	AAT	216
CAG	TGG	 	TAC	CAA	CGT	ccr	GGG	GGA	AGA	ere	GTC	AGC	CTG				
Q	W	F	¥	Q	Ř	P	G	G	R	L	v	s	L	L	Y	N	P
TCT	ദേദ	225 ACA	115	CAG	234 AGT	GGG	ADA	243 CTG	ACA	TCC	252 ACA	ACA	GTC	261 ATT		GAA	270 CGT
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s	G	Ţ	K	Q	s	G	R	L	Ţ	S	T	T	٧	I	ĸ	E	R
CGC	AGC	279 mcm	mmc	CAC	288	mcc	mcc	297	CNG	a mc	306 ACA	GAC	ΨCA	315 GGC	ستب	ጥልጥ	324 CTC
		TCT			A11												
R	S	s	ŗ	Н	I	S	s	S	Q	I	T	D	s	G	T	Y	L
		333			342			351			360			369			378
TGT	GCC	TCA	TAA	TCT	GGA	GGA	AGC	AAT	GCA	AAG	CTA	ACC	TTC	GGG	AAA	GGC	ACT
C	A	s	N	s	G	G	s	N	A	K	L	T	F	G	ĸ	G	T
		387			396			4 C 5			414			423	Bann	F	432
AAA	CTC	TCT	GTT	AAA	TCA	GGT	GGC	GGA	GGG	TCT	GGC	GGG	GGT	GGA	TCC	GGG	GGT
K	L	s	v	ĸ	s	<u>G</u>	G	G	G	s		G		G_	_ <u>s</u> _	G_	G
		441			450			459		Ţ	- i N'	Kei	ک	477			486
GGA	GGC		GAG	GCT	450 GCA	GTC	ACC			CCA			AAG		GCA	GTA	
- 											- R			 V		 V	T
<u>G</u>	<u>G</u>	s	Ŀ	Α	A	V	T	Q	s	P	K	N	Λ.	•	^	•	
CC 1		495	CTC.	ACA	504	200	m c m	513	CNC	እ ርጣ	522 ייית מ	220	CAC	531		ATG	540 TAC
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166	TAT	CGG	CAG	GAC	ACG	GGG	CAT			AGG		AIC	CAT	TAI			
W	Y	R	Q	ב	T	G	Н	G	L	R	L	I	Н	Y	s	Y	G
		603	_	_	612			621			630			639			641
GCT	GGC	AGC		GAG			GAT										
А	ؿ	š	7	Ε	ĸ	G	D	I	P	D	G	Y	ĸ	Λ	s	R	P

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					AGC					AC.	AAC		AGA			110	GGT		
ν	Y	F	С	А	s	G	Ε	т	G	Ţ	n	Ε	R	L	F	F	G		
Chm	CCA	765	220	ama	774 mcm	c m c	cmc	7834	<u>ع جر</u>		792			801	mm a		810		
CAI		ACC	AAG	CTG	TCT	GTC	CTG	ACT	AGT	AAC	TCC	ATC	ATG	TAC	TTC	AGC	CAC		
н	G	T	K	L	S	v	L	T	s	N	s	I	М	Y	F	s	н		
mon c	ama	819	cm.c	ann a	828	223	255	837	222		846			855	222		864	CD (2)	
			G1.C	110	CIG	CCA		AAG		ACC	ACG	ACG	CCA	GCG		CGA	CCA	CDR	HINGE
F	v	P	v	F	L	P	A	ĸ	P	T	Ţ.	T	P	A	P	R	P		
~~>		873		~~~	882			891			900			909			918		
CCA	ACA	CCG	GCG	aaa	ACC	ATC	GCG	TCG	CAG	ccc	CTG	TCC	CIG	CGC	CCA	TCT	AGT		
P	Ţ.	P	А	P	т	I	A	s	Q	P	L	s	L.	R	p	s	s		
	_								-										
	<u> </u>				936			945			954			963			972		
	AGA	GAT	ccc	AAA	CTC	TGC	TAC	CTG	CTG	GAT	GGA	ATC	CIC	TTC	ATC	TAT	GGT		
S	R		P	к	L	С	Y	L	L	D	G	I	L	F	I	Y	G		
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: É		981			990			999			1008			1017			1026		
GTC	ATT	CTC	ACT	GCC	TTG	TTC	CTG	AGA	GTG	AAG	TTC	AGC	AGG	AGC	GCA	GAC	GCC		
V	I	7.	T	A	L	F	L	R	v	v	F	s	R	s	A	D	Α		
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	1	.035			1044			1053			1062			1071			1080		
GCC	GCG	TAC	CAG	CAG	GGC	CAG	AAC	CAG	CTC		CAA	GAG	crc	AAT	CTA	GGA	CGA		
P	A	Y	Q	Q	G	Q	N	Q	L	Y	N	E	L	N	L	G	R	$\overline{}$	
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	1	.305		1	1314		2	323			1332		7	£311	<u> </u>		1350		
TAC	GAC	GCC	CTT	CAC	ATG	CAG	GCC	CTG	CCC	CCT	CGC	TAA	GCG	GCC	GCC	ACC	GCG		
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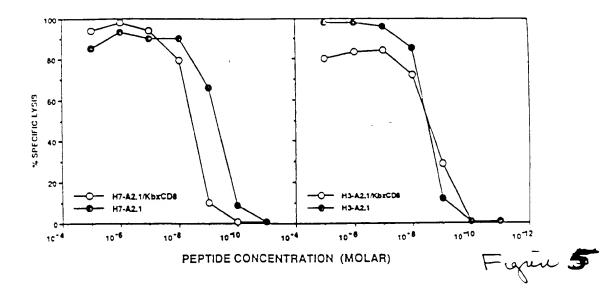


FIGURE STATE

CCC AAG GCA CTG ATG TTC ATC TT √α2 TGA GAC AAA GTC CCC AAT CTC TGA CAG Vα3

CTG CAG CTG CTC CTC AAG TAC TAT TC Va4.1.2.3 TCC CGG AGA AGG TCC ACA GTT CCT CTT T Vα4 4 GAA GCA GCA GAG GGT TTG AAG CCA CAT AC

	2 .	·
	Va5	GGC AGG TCT TCA GTT GCT TAT GAA GGT
,	Va6	GGT TCC TCT TCA GGG TCC AGA ATA TGT
	Va7	GCG AAG AAC TCA CCC TGG ACT GTT CAT
	Va8	GAG CTC CAC AGA CAA CAA GAG GAC CGA GCA
	Vα9	GAG CTG CGA CGT TCC TTA GTG ACT GTG
	3	· V
	Val0	CCT CGT CAG CCT GTT GTC CAA TCC TTC TGG
	Vall	CA'G CCT CAT CAA TCT GTT CTA CTT GGC T
	Vα12	CCA CCA GGG ACC ACA GTT TAT CAT TCA A
	Val4	ACC TOG AGA GAA TCC TAA GCT CAT CAT
	Va15	AGG TCT/TGT GTC CCT GAC AGT CCT GGT T
	4.	\
	Ψ. Val6	CAA CCA A C C C C C C C C C C C C C C C
		CAA GCA AAC ACT GTA GTG CAG AGC CCT TCC
	Vα17	CAA GAC ATC CAT AAC TGC CCT ACA G
	Vα18	GTG TAT GAA ACC CAG GAC AGT TCT TAC
	Vα19	CCG TAT TTC TTT CTT ATG TTG TTT TGG AT
	Va20	CAA AGC TCT CCA TCG CTG ACT GTT CAA G
	Beta Group	
	Beta Group	0.5

VB1	ATC TAA TCC TGG GAA GAG CAA AT
Vβ2	GGC GTC TGG TAC CAC GTG GTC AA
VB3	GTG AAA GGG CAA GGA CAA AAA GC
Vß4	GAT ATG CGA ACA GTA TCT AGG C
Vβ5.1	ACA TAA TCA AAQ GAA AGG GAG AA

VB6	TCC TGA TTG GTC AGG AAG GGC AA
VB7	TAC CTG ATC AAA AGA ATG GGA GA
VB8.1	ATA ACC ATG ACA ATA TOT ACT GG
VB8.2	ATA ACC ACA ACA ACA TGT ACT GG
VB8.3	ATA GCC ACA ACT ACT TGT ACT GG

3.	\bigwedge
Vβ9	AGC TTG CAA GAG TTG GAA AAC CA
VBIO	GAT TAT GTT TAG CTA CAA TAA TA
VB11	ACA AGG TGA CAG GGA AGG GAC AA
VB12	ACC TAC AGA ACC CAA GGA CTC AG
VB13	CAG TTG CCC TCG GAT CGA TTT TC

4.	\
VB14	GCC GAG ATC AAG GCT GTG GGC AG
VB15	AGA ACC ATC TGT AAG AGT GGA AC
VB16	CAT CAA ATA ATA GAT ATG GGG CA
Vβ17	GTA GTC CTG AAA AAG GGC ACA CT
VB18	CAT CTG TCA AAG TGG CAC TTC A

le Name : SEQ-<u>H7-ALPHA-1</u> ange : 1 - 393 adon Table : Universal



ATG	AAA	9 TCC	TTG	AGT	18 GTT	TCC	СТА	27 GTG	стc	CTG	36 TGG	СТС	CAG	45 TTA	AAC	TGG	54 GTG
Met	Lys	Ser	Leu	Ser	Val	Ser	 Leu	Val	Val	Leu	Trp	Leu	Gln	Leu	Asn	Trp	Val
CAG	AGC	63 (AG			72 GT G												108 GGA
Gln	Ser	Gln	Gln	Lys	Val	Gln	Gln	Ser	Pro	Glu	Ser	Leu	Ser	Val	Pro	Glu	Gly
GGC	ATG	117 GCC	TCT		126 AAC	TGC	ACT	135 TCA	AGT	GAT	144 CGC	AAT	ПП 	153 CAG	TAT	πс	162 TGG
Gly	Met	Ala	Ser	Leu	Asn	Cys	Thr	Ser	Ser	Asp	Arg	Asn	Phe	Gln	Tyr	Phe	Trp
TGG	TAC	171 AGA	CAG														216 TCT
Trp	Tyr	Arg	Gln	His	Ser	Gly	Glu	Gly	Pro	Lys	Ala	Leu	Met	Ser	Ile	Phe	Ser
GAT	GGT	225 GAC	AAG	AAA	234 Gaa	GGC	AGA	243 TTC	ACA	GCT	252 CAC	стс	AAT	261 AAG	GCC	AGC	27 0 CT G
Asp	Gly	Asp	Lys	Lys	Glu	Gly	Arg	Phe	Thr	Ala	His	Leu	Asn	Lys	Ala	Ser	Leu
CAT	GTT	27 9 TCC			288 ATC												324 TTC
His	Val	Ser	Leu	His	Ile	Arg	Asp	Ser	Gln	Pro	Ser	Asp	Ser	Ala	Leu	Tyr	Phe
TGT	GCA	333 GTT	ATG		342 TAT									369 CAG			378 AAG

Cys Ala Val Met Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys

387
TTA TCT ATC AAG CCC 3'
Leu Ser Ile Lys Pro

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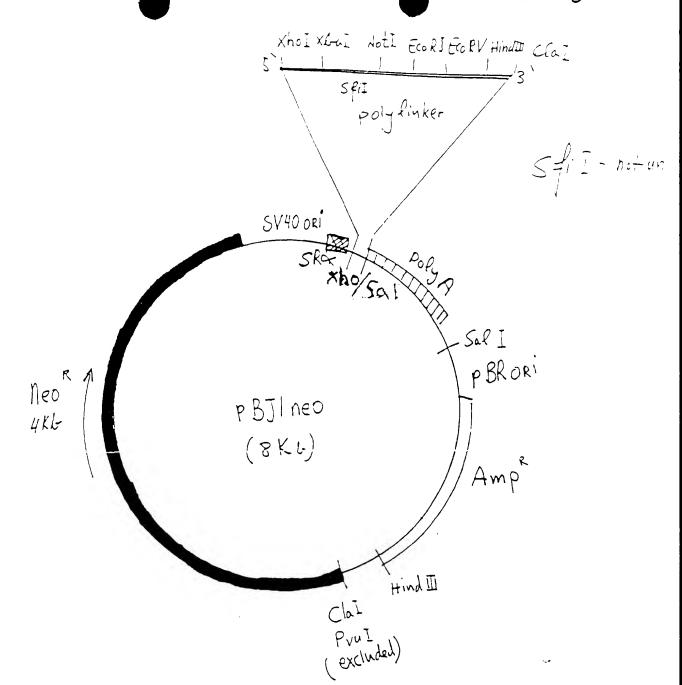
DNA Franslation [h7-beta] le Name : h7-beta

402 odon Table : Universal

: Normal

716 7B

08/8199 18 27 45 36 ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA CAC ATG Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys His Met GAG GCT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA ACA GGA GGA AAG Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val Thr Gly Gly Lys 126 135 144 GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC TAT ATG TAC TGG TAT CGG Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp Tyr Met Tyr Trp Tyr Arg 189 CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAC TCA TAT GTC GCT GAC AGC Gln Asp Thr Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Val Ala Asp Ser 234 243 ACG GAG AAA GGA GAT ATC CCT GAT GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG Thr Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu 288 **297** 306 AAT TTC TCT CTC ATT CTG GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC Asn Phe Ser Leu Ile Leu Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe 342 351 369 TGT GCC AGC AGC GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT Cys Ala Ser Ser Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly 396 CCC GGC ACC AGG CTC ACG GTT TCT 3' Pro Gly Thr Arg Leu Thr Val Ser



Ref:

pBJI meo - MCB 8: 466, 1988

Polylinker- Science, 249: 677, 1990

